

SEQUENCE LISTING

<110> Tsukahara, Kappei
 Tsuchiya, Mamiko
 Jigami, Yoshifumi
 Nakayama, Kenichi
 Umemura, Mariko
 Okamoto, Michiyo

<120> METHOD OF SCREENING FOR COMPOUNDS THAT
 INHIBIT THE ENZYMATIC ACTIVITY OF GWT1 GENE PRODUCT

<130> 082368-004400US

<140> 10/536,935

<141>

<150> PCT/JP03/14909

<151> 2003-11-21

<150> JP 2002-339418

<151> 2002-11-22

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1497

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1494)

<400> 1

atg gca aca gta cat cag aag aat atg tcg act tta aaa cag aga aaa	48
Met Ala Thr Val His Gln Lys Asn Met Ser Thr Leu Lys Gln Arg Lys	
1 5 10 15	
gag gac ttt gtg aca ggg ctc aat ggc ggt tct ata aca gaa att aac	96
Glu Asp Phe Val Thr Gly Leu Asn Gly Gly Ser Ile Thr Glu Ile Asn	
20 25 30	
gca gtg aca tca att gct ttg gta act tac ata tca tgg aac tta ttg	144
Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu	
35 40 45	
aaa aat tcc aac ctt atg cct cct ggc att tcc agc gtg caa tac ata	192
Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile	
50 55 60	
att gat ttt gca ttg aac tgg gtt gct ttg ctt cta tct att act att	240
Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Ser Ile Thr Ile	
65 70 75 80	
tat gct agt gaa cca tac ctt cta aac acg cta ata ctg tta cct tgt	288
Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys	

85										90					95					
ttg	ctc	gca	ttc	ata	tat	gga	aaa	ttt	act	agc	tcg	agt	aaa	cct	tct	336				
Leu	Leu	Ala	Phe	Ile	Tyr	Gly	Lys	Phe	Thr	Ser	Ser	Ser	Lys	Pro	Ser					
			100					105					110							
aat	cca	ata	tac	aat	aaa	aaa	aaa	atg	att	aca	cag	cgg	ttc	caa	cta	384				
Asn	Pro	Ile	Tyr	Asn	Lys	Lys	Lys	Met	Ile	Thr	Gln	Arg	Phe	Gln	Leu					
		115					120					125								
gaa	aaa	aag	ccg	tat	att	act	gcg	tat	cgt	ggt	ggg	atg	ctt	att	ctg	432				
Glu	Lys	Lys	Pro	Tyr	Ile	Thr	Ala	Tyr	Arg	Gly	Gly	Met	Leu	Ile	Leu					
	130					135					140									
act	gct	att	gcc	atc	ttg	gct	gta	gat	ttt	cca	att	ttc	cca	agg	agg	480				
Thr	Ala	Ile	Ala	Ile	Leu	Ala	Val	Asp	Phe	Pro	Ile	Phe	Pro	Arg	Arg					
145					150					155					160					
ttt	gcc	aag	gtg	gaa	act	tgg	ggg	aca	tcc	ctg	atg	gat	ctt	ggt	gta	528				
Phe	Ala	Lys	Val	Glu	Thr	Trp	Gly	Thr	Ser	Leu	Met	Asp	Leu	Gly	Val					
			165						170					175						
gga	tca	ttc	gtt	ttc	agt	aac	ggt	att	gtt	tct	tct	agg	gca	ctg	ttg	576				
Gly	Ser	Phe	Val	Phe	Ser	Asn	Gly	Ile	Val	Ser	Ser	Arg	Ala	Leu	Leu					
			180					185					190							
aaa	aac	cta	agc	ttg	aag	agt	aaa	ccc	agc	ttc	tta	aaa	aat	gca	ttt	624				
Lys	Asn	Leu	Ser	Leu	Lys	Ser	Lys	Pro	Ser	Phe	Leu	Lys	Asn	Ala	Phe					
		195					200					205								
aat	gcc	tta	aaa	tca	gga	gga	act	cta	ttg	ttc	cta	gga	ttg	ctg	agg	672				
Asn	Ala	Leu	Lys	Ser	Gly	Gly	Thr	Leu	Leu	Phe	Leu	Gly	Leu	Leu	Arg					
	210					215					220									
ttg	ttt	ttt	gta	aaa	aat	ttg	gaa	tat	caa	gaa	cat	gtc	aca	gaa	tat	720				
Leu	Phe	Phe	Val	Lys	Asn	Leu	Glu	Tyr	Gln	Glu	His	Val	Thr	Glu	Tyr					
225					230					235					240					
ggg	gtt	cat	tgg	aat	ttt	ttt	atc	acc	cta	tca	ttg	ttg	cca	ctt	gta	768				
Gly	Val	His	Trp	Asn	Phe	Phe	Ile	Thr	Leu	Ser	Leu	Leu	Pro	Leu	Val					
				245					250					255						
ttg	acc	ttt	att	gat	ccc	gtc	aca	aga	atg	gtt	cca	cgc	tgc	tca	att	816				
Leu	Thr	Phe	Ile	Asp	Pro	Val	Thr	Arg	Met	Val	Pro	Arg	Cys	Ser	Ile					
			260					265					270							
gca	ata	ttc	att	tca	tgc	att	tat	gaa	tgg	cta	ctt	tta	aag	gac	gat	864				
Ala	Ile	Phe	Ile	Ser	Cys	Ile	Tyr	Glu	Trp	Leu	Leu	Leu	Lys	Asp	Asp					
		275					280					285								
cgc	act	tta	aac	ttt	tta	att	ttg	gct	gat	aga	aat	tgt	ttc	ttc	agt	912				
Arg	Thr	Leu	Asn	Phe	Leu	Ile	Leu	Ala	Asp	Arg	Asn	Cys	Phe	Phe	Ser					
	290					295					300									
gct	aat	aga	gaa	ggc	atc	ttc	tca	ttt	cta	ggt	tat	tgc	tcg	att	ttt	960				
Ala	Asn	Arg	Glu	Gly	Ile	Phe	Ser	Phe	Leu	Gly	Tyr	Cys	Ser	Ile	Phe					
305					310					315					320					
ctt	tgg	ggc	caa	aac	acg	gga	ttt	tac	ttg	ttg	gga	aat	aaa	cca	act	1008				
Leu	Trp	Gly	Gln	Asn	Thr	Gly	Phe	Tyr	Leu	Leu	Gly	Asn	Lys	Pro	Thr					
				325					330					335						

tta aac aat ctt tat aag cct tct acg caa gac gta gtt gca gca tca	1056
Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser	
340 345 350	
aag aag tct tcg act tgg gac tat tgg act tca gta acc cca tta agt	1104
Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser	
355 360 365	
ggc ctc tgt ata tgg agt aca att ttt ctt gtt atc agc cag ttg gtt	1152
Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val	
370 375 380	
ttt caa tac cat cct tat agt gtt tca aga agg ttt gct aac tta cca	1200
Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro	
385 390 395 400	
tat act ttg tgg gtc att act tat aat tta cta ttt ttg act ggg tac	1248
Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr	
405 410 415	
tgc ttg act gac aaa att ttc ggt aat tct tcg gaa tat tat aaa gtt	1296
Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val	
420 425 430	
gcc gaa tgc ttg gaa tca atc aac tcc aat ggg ttg ttt tta ttt ttg	1344
Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu	
435 440 445	
ttg gca aat gtc tct act ggt tta gtc aat atg tct atg gtc acg ata	1392
Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile	
450 455 460	
gat tct tca ccc tta aaa tca ttc ctg gtt ttg ttg gca tac tgc tca	1440
Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser	
465 470 475 480	
ttc ata gct gtc ata tcg gtt ttc ttg tat aga aaa aga ata ttc att	1488
Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile	
485 490 495	
aag cta taa	1497
Lys Leu	

<210> 2
 <211> 498
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 2
 Met Ala Thr Val His Gln Lys Asn Met Ser Thr Leu Lys Gln Arg Lys
 1 5 10 15
 Glu Asp Phe Val Thr Gly Leu Asn Gly Gly Ser Ile Thr Glu Ile Asn
 20 25 30
 Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu
 35 40 45

Lys	Asn	Ser	Asn	Leu	Met	Pro	Pro	Gly	Ile	Ser	Ser	Val	Gln	Tyr	Ile	50	55	60
Ile	Asp	Phe	Ala	Leu	Asn	Trp	Val	Ala	Leu	Leu	Leu	Ser	Ile	Thr	Ile	65	70	75
Tyr	Ala	Ser	Glu	Pro	Tyr	Leu	Leu	Asn	Thr	Leu	Ile	Leu	Leu	Pro	Cys	85	90	95
Leu	Leu	Ala	Phe	Ile	Tyr	Gly	Lys	Phe	Thr	Ser	Ser	Ser	Lys	Pro	Ser	100	105	110
Asn	Pro	Ile	Tyr	Asn	Lys	Lys	Lys	Met	Ile	Thr	Gln	Arg	Phe	Gln	Leu	115	120	125
Glu	Lys	Lys	Pro	Tyr	Ile	Thr	Ala	Tyr	Arg	Gly	Gly	Met	Leu	Ile	Leu	130	135	140
Thr	Ala	Ile	Ala	Ile	Leu	Ala	Val	Asp	Phe	Pro	Ile	Phe	Pro	Arg	Arg	145	150	155
Phe	Ala	Lys	Val	Glu	Thr	Trp	Gly	Thr	Ser	Leu	Met	Asp	Leu	Gly	Val	165	170	175
Gly	Ser	Phe	Val	Phe	Ser	Asn	Gly	Ile	Val	Ser	Ser	Arg	Ala	Leu	Leu	180	185	190
Lys	Asn	Leu	Ser	Leu	Lys	Ser	Lys	Pro	Ser	Phe	Leu	Lys	Asn	Ala	Phe	195	200	205
Asn	Ala	Leu	Lys	Ser	Gly	Gly	Thr	Leu	Leu	Phe	Leu	Gly	Leu	Leu	Arg	210	215	220
Leu	Phe	Phe	Val	Lys	Asn	Leu	Glu	Tyr	Gln	Glu	His	Val	Thr	Glu	Tyr	225	230	235
Gly	Val	His	Trp	Asn	Phe	Phe	Ile	Thr	Leu	Ser	Leu	Leu	Pro	Leu	Val	245	250	255
Leu	Thr	Phe	Ile	Asp	Pro	Val	Thr	Arg	Met	Val	Pro	Arg	Cys	Ser	Ile	260	265	270
Ala	Ile	Phe	Ile	Ser	Cys	Ile	Tyr	Glu	Trp	Leu	Leu	Leu	Lys	Asp	Asp	275	280	285
Arg	Thr	Leu	Asn	Phe	Leu	Ile	Leu	Ala	Asp	Arg	Asn	Cys	Phe	Phe	Ser	290	295	300
Ala	Asn	Arg	Glu	Gly	Ile	Phe	Ser	Phe	Leu	Gly	Tyr	Cys	Ser	Ile	Phe	305	310	315
Leu	Trp	Gly	Gln	Asn	Thr	Gly	Phe	Tyr	Leu	Leu	Gly	Asn	Lys	Pro	Thr	325	330	335
Leu	Asn	Asn	Leu	Tyr	Lys	Pro	Ser	Thr	Gln	Asp	Val	Val	Ala	Ala	Ser	340	345	350
Lys	Lys	Ser	Ser	Thr	Trp	Asp	Tyr	Trp	Thr	Ser	Val	Thr	Pro	Leu	Ser	355	360	365

Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val
 370 375 380
 Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro
 385 390 395 400
 Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr
 405 410 415
 Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val
 420 425 430
 Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu
 435 440 445
 Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile
 450 455 460
 Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser
 465 470 475 480
 Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile
 485 490 495
 Lys Leu

<210> 3
 <211> 1458
 <212> DNA
 <213> Candida albicans

<220>
 <221> CDS
 <222> (1)..(1455)

<400> 3
 atg tca tcg tct tta aaa caa ttg aaa gaa caa ttt gtc tca gat ttg 48
 Met Ser Ser Ser Leu Lys Gln Leu Lys Glu Gln Phe Val Ser Asp Leu
 1 5 10 15
 act ggt ggc aca att gaa gaa att tat gct gta acc agt ata gca tta 96
 Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu
 20 25 30
 tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta 144
 Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu
 35 40 45
 gct ttg att tac gac tac att ctt aat gtg ttg aca att cta gca tcc 192
 Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser
 50 55 60
 att act gtt tat agc aac agc cct tct tat ttg cat tat ttt att gtt 240
 Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val
 65 70 75 80
 att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca 288
 Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
 85 90 95

tct tca ccc cat aga caa aat gat aca aaa gaa gat aaa tcg gac gaa	336
Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu	
100 105 110	
cta ttg ccg aga aaa caa ttt ata aca gcc tat cgt tct caa atg ttg	384
Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu	
115 120 125	
ata att act aat cta gct ata tta gct gtt gat ttt cct att ttc cca	432
Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro	
130 135 140	
aga aga ttt gcc aaa gtg gaa aca tgg ggc acg tca atg atg gat tta	480
Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu	
145 150 155 160	
gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa	528
Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln	
165 170 175	
ttg atc aag aac cac acc gac aac tac aaa ttt agt tgg aag agt tat	576
Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr	
180 185 190	
ttg aaa aca atc aag cag aac ttt atc aag tca gtg cct ata ctt gtt	624
Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val	
195 200 205	
tta gga gct att cgt ttt gtt agt gtt aag caa ttg gac tat cag gaa	672
Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu	
210 215 220	
cac gaa aca gag tat gga atc cat tgg aat ttt ttc ttc aca tta ggg	720
His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Phe Thr Leu Gly	
225 230 235 240	
ttc ttg cca att gta ttg gga ata tta gac ccg gtg ttg aat ttg gtt	768
Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val	
245 250 255	
cca cgc ttc ata ata gga att ggt atc tca att gct tat gag gta gcg	816
Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Ala Tyr Glu Val Ala	
260 265 270	
ttg aat aag act ggt ttg ttg aag ttc att ttg agc agc gaa aac aga	864
Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg	
275 280 285	
ctt gaa tct ctc atc acc atg aat aaa gaa ggt att ttt tcg ttt att	912
Leu Glu Ser Leu Ile Thr Met Asn Lys Glu Gly Ile Phe Ser Phe Ile	
290 295 300	
gga tat ctt tgt att ttt ata att ggt cag tct ttt ggg tca ttt gtt	960
Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val	
305 310 315 320	
tta aca ggc tac aaa aca aag aac aac tta ata acc att agc aaa att	1008
Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile	
325 330 335	

cgt att tca aaa aaa caa cac aag aaa gag ctg ctg ctg ttt ttc tca 1056
 Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser
 340 345 350

gtc gcc act act cag gga tta tat ttg gca tgt atc ttc tat cac tta 1104
 Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu
 355 360 365

gct ttc agt ttg ttc atc agc aac tta tca ttc ttg caa cca att tca 1152
 Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser
 370 375 380

aga cga ttg gcc aat ttc ccc tac gtc atg tgg gtc gtt tcg tac aat 1200
 Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn
 385 390 395 400

gct acg ttt tta tta tgt tat gac tta att gaa aaa ttt atc ccg ggg 1248
 Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly
 405 410 415

aac ctt act tct act gta ttg gac tct att aat aac aat ggt tta ttt 1296
 Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe
 420 425 430

atc ttc ttg gtc agc aat tta tta aca ggg ttt att aac atg tcc atc 1344
 Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile
 435 440 445

aac act ttg gaa act agc aat aaa atg gca gtg att atc ttg att ggc 1392
 Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly
 450 455 460

tat agt ctt act tgg aca ttg ctc gcc tta tat ttg gat aag agg aag 1440
 Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys
 465 470 475 480

atc tac atc aag ctt tag 1458
 Ile Tyr Ile Lys Leu
 485

<210> 4
 <211> 485
 <212> PRT
 <213> Candida albicans

<400> 4
 Met Ser Ser Ser Leu Lys Gln Leu Lys Glu Gln Phe Val Ser Asp Leu
 1 5 10 15

Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu
 20 25 30

Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu
 35 40 45

Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser
 50 55 60

Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val

385 390 395 400

Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly
 405 410 415

Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe
 420 425 430

Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile
 435 440 445

Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly
 450 455 460

Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys
 465 470 475 480

Ile Tyr Ile Lys Leu
 485

<210> 5
 <211> 1458
 <212> DNA
 <213> Candida albicans

<220>
 <221> CDS
 <222> (1)..(1455)

<400> 5
 atg tca tcg tct tta aaa caa ttg aaa gaa caa ttt gtc tca gat ttg 48
 Met Ser Ser Ser Leu Lys Gln Leu Lys Glu Gln Phe Val Ser Asp Leu
 1 5 10 15

act ggt ggc aca att gaa gaa att tat gct gta acc agt ata gca tta 96
 Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu
 20 25 30

tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta 144
 Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu
 35 40 45

gct ttg att tac gac tac att ctt aat gtg ttg aca att cta gca tcc 192
 Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser
 50 55 60

att act gtt tat agc aac agc cct tct tat ttg cat tat ttt att gtt 240
 Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val
 65 70 75 80

att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca 288
 Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
 85 90 95

tct tca ccc cat aga caa aat gat aca aaa gaa gat aaa tcg gac gaa 336
 Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu
 100 105 110

cta ttg ccg aga aaa caa ttt ata aca gcc tat cgt tct caa atg ttg 384
 Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu

115						120						125						
ata	att	act	aat	cta	gct	ata	tta	gct	gtt	gat	ttt	cct	att	ttc	cca	432		
Ile	Ile	Thr	Asn	Leu	Ala	Ile	Leu	Ala	Val	Asp	Phe	Pro	Ile	Phe	Pro			
130						135						140						
aga	aga	ttt	gcc	aaa	gtg	gaa	aca	tgg	ggc	acg	tca	atg	atg	gat	tta	480		
Arg	Arg	Phe	Ala	Lys	Val	Glu	Thr	Trp	Gly	Thr	Ser	Met	Met	Asp	Leu			
145						150						155						160
gga	gtt	ggg	tcg	ttt	gtg	ttc	tcc	atg	ggg	ttg	gct	aat	tct	cga	caa	528		
Gly	Val	Gly	Ser	Phe	Val	Phe	Ser	Met	Gly	Leu	Ala	Asn	Ser	Arg	Gln			
165						170						175						
ttg	atc	aag	aac	cac	acc	gac	aat	tac	aaa	ttt	agt	tgg	aag	agt	tat	576		
Leu	Ile	Lys	Asn	His	Thr	Asp	Asn	Tyr	Lys	Phe	Ser	Trp	Lys	Ser	Tyr			
180						185						190						
ttg	aaa	aca	atc	aag	cag	aac	ttt	atc	aag	tca	gtg	cct	ata	ctt	gtt	624		
Leu	Lys	Thr	Ile	Lys	Gln	Asn	Phe	Ile	Lys	Ser	Val	Pro	Ile	Leu	Val			
195						200						205						
tta	gga	gct	att	cgt	ttt	gtt	agt	gtt	aag	caa	ttg	gac	tat	cag	gaa	672		
Leu	Gly	Ala	Ile	Arg	Phe	Val	Ser	Val	Lys	Gln	Leu	Asp	Tyr	Gln	Glu			
210						215						220						
cac	gaa	aca	gag	tat	gga	atc	cat	tgg	aat	ttt	ttc	ttc	aca	tta	ggg	720		
His	Glu	Thr	Glu	Tyr	Gly	Ile	His	Trp	Asn	Phe	Phe	Phe	Thr	Leu	Gly			
225						230						235						240
ttc	ttg	cca	att	gta	ttg	gga	ata	tta	gac	ccg	gtg	ttg	aat	ttg	gtt	768		
Phe	Leu	Pro	Ile	Val	Leu	Gly	Ile	Leu	Asp	Pro	Val	Leu	Asn	Leu	Val			
245						250						255						
cca	cgc	ttc	ata	ata	gga	att	ggt	atc	tca	att	ggt	tat	gag	gta	gcg	816		
Pro	Arg	Phe	Ile	Ile	Gly	Ile	Gly	Ile	Ser	Ile	Gly	Tyr	Glu	Val	Ala			
260						265						270						
ttg	aat	aag	act	ggt	ttg	ttg	aag	ttc	att	ttg	agc	agc	gaa	aac	aga	864		
Leu	Asn	Lys	Thr	Gly	Leu	Leu	Lys	Phe	Ile	Leu	Ser	Ser	Glu	Asn	Arg			
275						280						285						
ctt	gaa	tct	ctc	atc	gcc	atg	aat	aaa	gaa	ggt	att	ttt	tcg	ttt	att	912		
Leu	Glu	Ser	Leu	Ile	Ala	Met	Asn	Lys	Glu	Gly	Ile	Phe	Ser	Phe	Ile			
290						295						300						
gga	tat	ctt	tgt	att	ttt	ata	att	ggt	cag	tct	ttt	ggg	tca	ttt	gtt	960		
Gly	Tyr	Leu	Cys	Ile	Phe	Ile	Ile	Gly	Gln	Ser	Phe	Gly	Ser	Phe	Val			
305						310						315						320
tta	aca	ggc	tac	aaa	aca	aag	aac	aac	tta	ata	acc	att	agc	aaa	att	1008		
Leu	Thr	Gly	Tyr	Lys	Thr	Lys	Asn	Asn	Leu	Ile	Thr	Ile	Ser	Lys	Ile			
325						330						335						
cgt	att	tca	aaa	aaa	caa	cac	aag	aaa	gag	ctg	ctg	ctg	ttt	ttc	tca	1056		
Arg	Ile	Ser	Lys	Lys	Gln	His	Lys	Lys	Glu	Leu	Leu	Leu	Phe	Phe	Ser			
340						345						350						
gtc	gcc	act	act	cag	gga	tta	tat	ttg	gca	tgt	atc	ttc	tat	cac	tta	1104		
Val	Ala	Thr	Thr	Gln	Gly	Leu	Tyr	Leu	Ala	Cys	Ile	Phe	Tyr	His	Leu			
355						360						365						

gct ttc agt ttg ttc atc agc aac tta tca ttc ttg caa cca att tca 1152
 Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser
 370 375 380

aga cga ttg gcc aat ttc ccc tac gtc atg tgg gtc gtt tcg tac aat 1200
 Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn
 385 390 395 400

gct acg ttt tta tta tgt tat gac tta att gaa aaa ttt atc ccg ggg 1248
 Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly
 405 410 415

aac ctt act tct act gta ttg gac tct att aat aac aat ggt tta ttt 1296
 Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe
 420 425 430

atc ttc ttg gtc agc aat tta tta aca ggg ttt att aac atg tcc atc 1344
 Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile
 435 440 445

aac act ttg gaa act agc aat aaa atg gca gtg att atc ttg att ggc 1392
 Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly
 450 455 460

tat agt ctt act tgg aca ttg ctc gcc tta tat ttg gat aag agg aag 1440
 Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys
 465 470 475 480

atc tac atc aag ctt tag 1458
 Ile Tyr Ile Lys Leu
 485

<210> 6

<211> 485

<212> PRT

<213> Candida albicans

<400> 6

Met Ser Ser Ser Leu Lys Gln Leu Lys Glu Gln Phe Val Ser Asp Leu
 1 5 10 15

Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu
 20 25 30

Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu
 35 40 45

Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser
 50 55 60

Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val
 65 70 75 80

Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
 85 90 95

Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu
 100 105 110

Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu
 115 120 125
 Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro
 130 135 140
 Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu
 145 150 155 160
 Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln
 165 170 175
 Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr
 180 185 190
 Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val
 195 200 205
 Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu
 210 215 220
 His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Phe Thr Leu Gly
 225 230 235 240
 Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val
 245 250 255
 Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Gly Tyr Glu Val Ala
 260 265 270
 Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg
 275 280 285
 Leu Glu Ser Leu Ile Ala Met Asn Lys Glu Gly Ile Phe Ser Phe Ile
 290 295 300
 Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val
 305 310 315 320
 Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile
 325 330 335
 Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser
 340 345 350
 Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu
 355 360 365
 Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser
 370 375 380
 Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn
 385 390 395 400
 Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly
 405 410 415
 Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe
 420 425 430
 Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile

435 440 445
 Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly
 450 455 460

 Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys
 465 470 475 480

 Ile Tyr Ile Lys Leu
 485

<210> 7
 <211> 1380
 <212> DNA
 <213> Schizosaccharomyces pombe

<220>
 <221> CDS
 <222> (1)..(1380)

<400> 7
 atg tca tac aaa ttg gaa aaa gaa gca ttt gtc tca aac ctg acg ggt 48
 Met Ser Tyr Lys Leu Glu Lys Glu Ala Phe Val Ser Asn Leu Thr Gly
 1 5 10 15

 tca agt tcc att gag aca tgt ggc ttg tta tta ata gga att gct tgc 96
 Ser Ser Ser Ile Glu Thr Cys Gly Leu Leu Leu Ile Gly Ile Ala Cys
 20 25 30

 aac gtt ttg tgg gta aac atg act gcg aga aac atc tta ccc aaa ggg 144
 Asn Val Leu Trp Val Asn Met Thr Ala Arg Asn Ile Leu Pro Lys Gly
 35 40 45

 aat ctt ggg ttt ctt gtt gag ttt ttc atc ttt tgc tta att cca tta 192
 Asn Leu Gly Phe Leu Val Glu Phe Phe Ile Phe Cys Leu Ile Pro Leu
 50 55 60

 ttt gtc att tac gtt tca tcg aaa gtt ggc gtt ttc act ctt tgc ata 240
 Phe Val Ile Tyr Val Ser Ser Lys Val Gly Val Phe Thr Leu Cys Ile
 65 70 75 80

 gcc tct ttt ttg cct tcc ttc gtc ctt cat gtt ata agt cca att aat 288
 Ala Ser Phe Leu Pro Ser Phe Val Leu His Val Ile Ser Pro Ile Asn
 85 90 95

 tgg gat gtg ctg aga aga aaa cct ggt tgt tgt ctt act aaa aaa aat 336
 Trp Asp Val Leu Arg Arg Lys Pro Gly Cys Cys Leu Thr Lys Lys Asn
 100 105 110

 gaa aat act ttt gat cga cga att gct gga gtc aca ttt tat cgt tct 384
 Glu Asn Thr Phe Asp Arg Arg Ile Ala Gly Val Thr Phe Tyr Arg Ser
 115 120 125

 caa atg atg ttg gtt act gtc act tgc atc ctg gcc gtt gac ttt acc 432
 Gln Met Met Leu Val Thr Val Thr Cys Ile Leu Ala Val Asp Phe Thr
 130 135 140

 ctt ttc ccg agg aga tat gcc aaa gtt gaa acc tgg gga aca tca ctg 480
 Leu Phe Pro Arg Arg Tyr Ala Lys Val Glu Thr Trp Gly Thr Ser Leu

145	150	155	160	
atg gat ctt ggt gtt gga tct ttc atg ttt tct tca ggt act gtg gct	Met Asp Leu Gly Val Gly Ser Phe Met Phe Ser Ser Gly Thr Val Ala	528		
	165 170 175			
gga cgg aaa aat gac att aaa aaa cca aat gcg ttt aaa aat gta ttg	Gly Arg Lys Asn Asp Ile Lys Lys Pro Asn Ala Phe Lys Asn Val Leu	576		
	180 185 190			
tgg aat tct ttc atc ctt ttg att tta gga ttt gcg cgc atg ttt tta	Trp Asn Ser Phe Ile Leu Leu Ile Leu Gly Phe Ala Arg Met Phe Leu	624		
	195 200 205			
acg aaa agc atc aat tac caa gaa cat gta agc gaa tat ggc atg cat	Thr Lys Ser Ile Asn Tyr Gln Glu His Val Ser Glu Tyr Gly Met His	672		
	210 215 220			
tgg aac ttt ttt ttc acc cta ggt ttc atg gct ctt ggc gta ttt ttt	Trp Asn Phe Phe Phe Thr Leu Gly Phe Met Ala Leu Gly Val Phe Phe	720		
	225 230 235 240			
ttt cgt cgt tct tta aaa aaa gtc tcc tat ttt aat tta gca acc ttc	Phe Arg Arg Ser Leu Lys Lys Val Ser Tyr Phe Asn Leu Ala Thr Phe	768		
	245 250 255			
att act ctt ctt cat cat tgt ttg ctt gtt tta acc cct ttc caa aaa	Ile Thr Leu Leu His His Cys Leu Leu Val Leu Thr Pro Phe Gln Lys	816		
	260 265 270			
tgg gca cta tcc gcc ccc aga aca aat att ttg gct cag aat aga gag	Trp Ala Leu Ser Ala Pro Arg Thr Asn Ile Leu Ala Gln Asn Arg Glu	864		
	275 280 285			
ggt att gct tct ctt ccc gga tac att gct att tac ttt tat gga atg	Gly Ile Ala Ser Leu Pro Gly Tyr Ile Ala Ile Tyr Phe Tyr Gly Met	912		
	290 295 300			
tat acc ggt agt gta gtt ttg gct gat cga cct cta atg tat act aga	Tyr Thr Gly Ser Val Val Leu Ala Asp Arg Pro Leu Met Tyr Thr Arg	960		
	305 310 315 320			
gct gag tcg tgg aag cgc ttt caa cgt cta tta ttc ccg cta tgc att	Ala Glu Ser Trp Lys Arg Phe Gln Arg Leu Leu Phe Pro Leu Cys Ile	1008		
	325 330 335			
ttg tta gtg ttg tat ctt gtg tct aac ttt ttg tca gtt ggt gtt tct	Leu Leu Val Leu Tyr Leu Val Ser Asn Phe Leu Ser Val Gly Val Ser	1056		
	340 345 350			
cgc cga ctt gct aat acg cct tat gtt gcg aat gtt gcc ttt atc aat	Arg Arg Leu Ala Asn Thr Pro Tyr Val Ala Asn Val Ala Phe Ile Asn	1104		
	355 360 365			
atg ttt ttt ctt act ata tac ata ctt att gat gcc tat tta ttc cca	Met Phe Phe Leu Thr Ile Tyr Ile Leu Ile Asp Ala Tyr Leu Phe Pro	1152		
	370 375 380			
tct tct gtg cca tat gga agt cgc gtc ccc aaa ctg ctt gaa gat gcc	Ser Ser Val Pro Tyr Gly Ser Arg Val Pro Lys Leu Leu Glu Asp Ala	1200		
	385 390 395 400			

aat aat aat ggc ttg ttg gtg ttt ttg att gct aac gtt tta aca gga	1248
Asn Asn Asn Gly Leu Leu Val Phe Leu Ile Ala Asn Val Leu Thr Gly	
405 410 415	
gta gtt aat tta tcg ttc gac acc ctt cat tct agc aat gca aaa ggc	1296
Val Val Asn Leu Ser Phe Asp Thr Leu His Ser Ser Asn Ala Lys Gly	
420 425 430	
ttg aca atc atg act atg tat ctt ttt att att tgc tat atg gca cat	1344
Leu Thr Ile Met Thr Met Tyr Leu Phe Ile Ile Cys Tyr Met Ala His	
435 440 445	
tgg ctt gct caa cac gga att cgt ttt cgc ctt tag	1380
Trp Leu Ala Gln His Gly Ile Arg Phe Arg Leu	
450 455	

<210> 8
 <211> 459
 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 8	
Met Ser Tyr Lys Leu Glu Lys Glu Ala Phe Val Ser Asn Leu Thr Gly	
1 5 10 15	
Ser Ser Ser Ile Glu Thr Cys Gly Leu Leu Leu Ile Gly Ile Ala Cys	
20 25 30	
Asn Val Leu Trp Val Asn Met Thr Ala Arg Asn Ile Leu Pro Lys Gly	
35 40 45	
Asn Leu Gly Phe Leu Val Glu Phe Phe Ile Phe Cys Leu Ile Pro Leu	
50 55 60	
Phe Val Ile Tyr Val Ser Ser Lys Val Gly Val Phe Thr Leu Cys Ile	
65 70 75 80	
Ala Ser Phe Leu Pro Ser Phe Val Leu His Val Ile Ser Pro Ile Asn	
85 90 95	
Trp Asp Val Leu Arg Arg Lys Pro Gly Cys Cys Leu Thr Lys Lys Asn	
100 105 110	
Glu Asn Thr Phe Asp Arg Arg Ile Ala Gly Val Thr Phe Tyr Arg Ser	
115 120 125	
Gln Met Met Leu Val Thr Val Thr Cys Ile Leu Ala Val Asp Phe Thr	
130 135 140	
Leu Phe Pro Arg Arg Tyr Ala Lys Val Glu Thr Trp Gly Thr Ser Leu	
145 150 155 160	
Met Asp Leu Gly Val Gly Ser Phe Met Phe Ser Ser Gly Thr Val Ala	
165 170 175	
Gly Arg Lys Asn Asp Ile Lys Lys Pro Asn Ala Phe Lys Asn Val Leu	
180 185 190	
Trp Asn Ser Phe Ile Leu Leu Ile Leu Gly Phe Ala Arg Met Phe Leu	

195	200	205
Thr Lys Ser Ile Asn Tyr Gln Glu His Val Ser Glu Tyr Gly Met His 210 215 220		
Trp Asn Phe Phe Phe Thr Leu Gly Phe Met Ala Leu Gly Val Phe Phe 225 230 235 240		
Phe Arg Arg Ser Leu Lys Lys Val Ser Tyr Phe Asn Leu Ala Thr Phe 245 250 255		
Ile Thr Leu Leu His His Cys Leu Leu Val Leu Thr Pro Phe Gln Lys 260 265 270		
Trp Ala Leu Ser Ala Pro Arg Thr Asn Ile Leu Ala Gln Asn Arg Glu 275 280 285		
Gly Ile Ala Ser Leu Pro Gly Tyr Ile Ala Ile Tyr Phe Tyr Gly Met 290 295 300		
Tyr Thr Gly Ser Val Val Leu Ala Asp Arg Pro Leu Met Tyr Thr Arg 305 310 315 320		
Ala Glu Ser Trp Lys Arg Phe Gln Arg Leu Leu Phe Pro Leu Cys Ile 325 330 335		
Leu Leu Val Leu Tyr Leu Val Ser Asn Phe Leu Ser Val Gly Val Ser 340 345 350		
Arg Arg Leu Ala Asn Thr Pro Tyr Val Ala Asn Val Ala Phe Ile Asn 355 360 365		
Met Phe Phe Leu Thr Ile Tyr Ile Leu Ile Asp Ala Tyr Leu Phe Pro 370 375 380		
Ser Ser Val Pro Tyr Gly Ser Arg Val Pro Lys Leu Leu Glu Asp Ala 385 390 395 400		
Asn Asn Asn Gly Leu Leu Val Phe Leu Ile Ala Asn Val Leu Thr Gly 405 410 415		
Val Val Asn Leu Ser Phe Asp Thr Leu His Ser Ser Asn Ala Lys Gly 420 425 430		
Leu Thr Ile Met Thr Met Tyr Leu Phe Ile Ile Cys Tyr Met Ala His 435 440 445		
Trp Leu Ala Gln His Gly Ile Arg Phe Arg Leu 450 455		

<210> 9
 <211> 1576
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <221> CDS
 <222> (31)..(1536)

<400> 9

aaggtgcaaa tcccgcgga ttgagtcaag atg gat cca gat tat aaa gct cgc	54
Met Asp Pro Asp Tyr Lys Ala Arg	
1 5	
aaa gag gcc ttt gtc tca ggt ctt gca gga gga agc atc ctg gaa atc	102
Lys Glu Ala Phe Val Ser Gly Leu Ala Gly Gly Ser Ile Leu Glu Ile	
10 15 20	
aac gcc gtc acc ttg gtt gct tcg gta tcc gtt ttt ctg tgg tca att	150
Asn Ala Val Thr Leu Val Ala Ser Val Ser Val Phe Leu Trp Ser Ile	
25 30 35 40	
cta caa tct cgc cta tcc ttt ttc aca ccc tac agc gcc gct gcc ctt	198
Leu Gln Ser Arg Leu Ser Phe Phe Thr Pro Tyr Ser Ala Ala Ala Leu	
45 50 55	
ctc gtt gat ttc ctg ctc aat gta cta gct atc ttg ttc gca acc act	246
Leu Val Asp Phe Leu Leu Asn Val Leu Ala Ile Leu Phe Ala Thr Thr	
60 65 70	
tta tac tct tcg gcg cct ctt ctt ctc aat ctc ctt cta ata tct ccc	294
Leu Tyr Ser Ser Ala Pro Leu Leu Leu Asn Leu Leu Leu Ile Ser Pro	
75 80 85	
gct ctg ctg ata ctc ctc tct acg aaa cgt cct cgg acc ccc gtc aaa	342
Ala Leu Leu Ile Leu Leu Ser Thr Lys Arg Pro Arg Thr Pro Val Lys	
90 95 100	
gcg aaa cct cct cgc cag tcc gct aga gct ggg aaa gat gac tcg aaa	390
Ala Lys Pro Pro Arg Gln Ser Ala Arg Ala Gly Lys Asp Asp Ser Lys	
105 110 115 120	
cat gcg aca gcc ttg cca gag tct cta ccc att cat cca ttt ctc acg	438
His Ala Thr Ala Leu Pro Glu Ser Leu Pro Ile His Pro Phe Leu Thr	
125 130 135	
aca tat cgc gcc gcc atg atg gtt atc acg tgc atc gct atc ttg gct	486
Thr Tyr Arg Ala Ala Met Met Val Ile Thr Cys Ile Ala Ile Leu Ala	
140 145 150	
gtg gat ttt cgc att ttt cct cgc cga ttc gcc aag gta gaa aac tgg	534
Val Asp Phe Arg Ile Phe Pro Arg Arg Phe Ala Lys Val Glu Asn Trp	
155 160 165	
ggt aca tca ctc atg gat ctg ggc gtt gga tcg ttt gtc ttt tcg ggc	582
Gly Thr Ser Leu Met Asp Leu Gly Val Gly Ser Phe Val Phe Ser Gly	
170 175 180	
gga gta gta tcc gct cgc tca cta ctc aag agc agg acc aat ggc tct	630
Gly Val Val Ser Ala Arg Ser Leu Leu Lys Ser Arg Thr Asn Gly Ser	
185 190 195 200	
aaa agg ttg cct ctt gcc aag agg ttg att gcg tcg acg cga cac tct	678
Lys Arg Leu Pro Leu Ala Lys Arg Leu Ile Ala Ser Thr Arg His Ser	
205 210 215	
att cct ctg ctc gtc ctc ggc ctg att cgg cta tac agc gtc aaa ggc	726
Ile Pro Leu Leu Val Leu Gly Leu Ile Arg Leu Tyr Ser Val Lys Gly	
220 225 230	
ttg gac tat gcg gag cac gtc acc gag tac ggc gta cat tgg aac ttc	774

Leu	Asp	Tyr	Ala	Glu	His	Val	Thr	Glu	Tyr	Gly	Val	His	Trp	Asn	Phe		
	235						240					245					
ttc	ttt	aca	ttg	ggt	ctt	ttg	cct	ccg	ttc	gtg	gag	gtc	ttc	gac	gcc	822	
Phe	Phe	Thr	Leu	Gly	Leu	Leu	Pro	Pro	Phe	Val	Glu	Val	Phe	Asp	Ala		
	250					255					260						
ttg	gct	acg	atc	att	ccg	tca	tac	gag	gtt	ctc	tcc	gtg	ggg	atc	gcc	870	
Leu	Ala	Thr	Ile	Ile	Pro	Ser	Tyr	Glu	Val	Leu	Ser	Val	Gly	Ile	Ala		
	265				270					275					280		
gtc	ttg	tat	caa	gtt	gcc	cta	gag	tca	aca	gac	ttg	aaa	agc	tac	atc	918	
Val	Leu	Tyr	Gln	Val	Ala	Leu	Glu	Ser	Thr	Asp	Leu	Lys	Ser	Tyr	Ile		
			285						290					295			
ctc	gtc	tcc	cct	cgt	ggg	cca	agc	tta	ctg	tcc	aag	aat	cgt	gaa	ggc	966	
Leu	Val	Ser	Pro	Arg	Gly	Pro	Ser	Leu	Leu	Ser	Lys	Asn	Arg	Glu	Gly		
			300					305					310				
gtc	ttc	tcc	ttc	tca	ggt	tat	ctc	gcg	att	ttt	ctt	gct	ggg	cgt	gcg	1014	
Val	Phe	Ser	Phe	Ser	Gly	Tyr	Leu	Ala	Ile	Phe	Leu	Ala	Gly	Arg	Ala		
		315					320					325					
atc	ggc	att	cgg	ata	atc	cct	cgc	gga	act	tct	ttc	tca	aga	agc	cca	1062	
Ile	Gly	Ile	Arg	Ile	Ile	Pro	Arg	Gly	Thr	Ser	Phe	Ser	Arg	Ser	Pro		
	330					335					340						
gaa	cag	gcc	agg	aga	cgg	gtc	ctg	atc	agc	ctt	ggc	gtg	caa	gcg	tta	1110	
Glu	Gln	Ala	Arg	Arg	Arg	Val	Leu	Ile	Ser	Leu	Gly	Val	Gln	Ala	Leu		
	345				350					355					360		
gtg	tgg	acc	act	ctt	ttt	gtg	ttg	aac	tcc	act	tat	gcg	atg	gga	tac	1158	
Val	Trp	Thr	Thr	Leu	Phe	Val	Leu	Asn	Ser	Thr	Tyr	Ala	Met	Gly	Tyr		
				365					370					375			
gga	gct	aat	atc	cct	gtc	tcc	cgc	cgc	ctc	gct	aac	atg	ccc	tat	gtc	1206	
Gly	Ala	Asn	Ile	Pro	Val	Ser	Arg	Arg	Leu	Ala	Asn	Met	Pro	Tyr	Val		
			380					385					390				
ctt	tgg	gtt	tcg	gcg	ttc	aac	acc	gcg	caa	ctg	ttt	gtg	ttc	tgc	ctg	1254	
Leu	Trp	Val	Ser	Ala	Phe	Asn	Thr	Ala	Gln	Leu	Phe	Val	Phe	Cys	Leu		
		395					400					405					
atc	gaa	aca	ctc	tgc	ttt	cct	gca	gtt	cat	cgg	aca	acg	act	caa	gag	1302	
Ile	Glu	Thr	Leu	Cys	Phe	Pro	Ala	Val	His	Arg	Thr	Thr	Thr	Gln	Glu		
	410					415					420						
agc	gaa	tct	gag	cga	gtc	gat	ttt	gct	acg	agc	cga	atc	atg	tcg	gcc	1350	
Ser	Glu	Ser	Glu	Arg	Val	Asp	Phe	Ala	Thr	Ser	Arg	Ile	Met	Ser	Ala		
	425				430					435					440		
ttc	aat	aag	aac	agt	ctc	gcg	atc	ttt	ctt	ttg	gcc	aat	ctt	ctg	act	1398	
Phe	Asn	Lys	Asn	Ser	Leu	Ala	Ile	Phe	Leu	Leu	Ala	Asn	Leu	Leu	Thr		
				445					450					455			
gga	gct	gtg	aat	ctg	agc	atc	tcc	aca	att	gat	gct	aat	aca	gcg	cag	1446	
Gly	Ala	Val	Asn	Leu	Ser	Ile	Ser	Thr	Ile	Asp	Ala	Asn	Thr	Ala	Gln		
			460					465					470				
gcc	atc	gct	gtt	ctc	att	gga	tat	tca	tcc	att	atc	aca	ggg	gtt	gct	1494	
Ala	Ile	Ala	Val	Leu	Ile	Gly	Tyr	Ser	Ser	Ile	Ile	Thr	Gly	Val	Ala		

475	480	485	
cta gca ttg cat cat gcc aat atc aaa gta ctt cct ttc tag			1536
Leu Ala Leu His His Ala Asn Ile Lys Val Leu Pro Phe			
490	495	500	
ggtattttacg agcaattggt ggtgtgttga agatatatag			1576
<210> 10			
<211> 501			
<212> PRT			
<213> Aspergillus fumigatus			
<400> 10			
Met Asp Pro Asp Tyr Lys Ala Arg Lys Glu Ala Phe Val Ser Gly Leu			
1	5	10	15
Ala Gly Gly Ser Ile Leu Glu Ile Asn Ala Val Thr Leu Val Ala Ser			
	20	25	30
Val Ser Val Phe Leu Trp Ser Ile Leu Gln Ser Arg Leu Ser Phe Phe			
	35	40	45
Thr Pro Tyr Ser Ala Ala Ala Leu Leu Val Asp Phe Leu Leu Asn Val			
	50	55	60
Leu Ala Ile Leu Phe Ala Thr Thr Leu Tyr Ser Ser Ala Pro Leu Leu			
	65	70	75
Leu Asn Leu Leu Leu Ile Ser Pro Ala Leu Leu Ile Leu Leu Ser Thr			
	85	90	95
Lys Arg Pro Arg Thr Pro Val Lys Ala Lys Pro Pro Arg Gln Ser Ala			
	100	105	110
Arg Ala Gly Lys Asp Asp Ser Lys His Ala Thr Ala Leu Pro Glu Ser			
	115	120	125
Leu Pro Ile His Pro Phe Leu Thr Thr Tyr Arg Ala Ala Met Met Val			
	130	135	140
Ile Thr Cys Ile Ala Ile Leu Ala Val Asp Phe Arg Ile Phe Pro Arg			
	145	150	155
Arg Phe Ala Lys Val Glu Asn Trp Gly Thr Ser Leu Met Asp Leu Gly			
	165	170	175
Val Gly Ser Phe Val Phe Ser Gly Gly Val Val Ser Ala Arg Ser Leu			
	180	185	190
Leu Lys Ser Arg Thr Asn Gly Ser Lys Arg Leu Pro Leu Ala Lys Arg			
	195	200	205
Leu Ile Ala Ser Thr Arg His Ser Ile Pro Leu Leu Val Leu Gly Leu			
	210	215	220
Ile Arg Leu Tyr Ser Val Lys Gly Leu Asp Tyr Ala Glu His Val Thr			
	225	230	235
			240

Glu Tyr Gly Val His Trp Asn Phe Phe Phe Thr Leu Gly Leu Leu Pro
 245 250 255
 Pro Phe Val Glu Val Phe Asp Ala Leu Ala Thr Ile Ile Pro Ser Tyr
 260 265 270
 Glu Val Leu Ser Val Gly Ile Ala Val Leu Tyr Gln Val Ala Leu Glu
 275 280 285
 Ser Thr Asp Leu Lys Ser Tyr Ile Leu Val Ser Pro Arg Gly Pro Ser
 290 295 300
 Leu Leu Ser Lys Asn Arg Glu Gly Val Phe Ser Phe Ser Gly Tyr Leu
 305 310 315 320
 Ala Ile Phe Leu Ala Gly Arg Ala Ile Gly Ile Arg Ile Ile Pro Arg
 325 330 335
 Gly Thr Ser Phe Ser Arg Ser Pro Glu Gln Ala Arg Arg Arg Val Leu
 340 345 350
 Ile Ser Leu Gly Val Gln Ala Leu Val Trp Thr Thr Leu Phe Val Leu
 355 360 365
 Asn Ser Thr Tyr Ala Met Gly Tyr Gly Ala Asn Ile Pro Val Ser Arg
 370 375 380
 Arg Leu Ala Asn Met Pro Tyr Val Leu Trp Val Ser Ala Phe Asn Thr
 385 390 395 400
 Ala Gln Leu Phe Val Phe Cys Leu Ile Glu Thr Leu Cys Phe Pro Ala
 405 410 415
 Val His Arg Thr Thr Thr Gln Glu Ser Glu Ser Glu Arg Val Asp Phe
 420 425 430
 Ala Thr Ser Arg Ile Met Ser Ala Phe Asn Lys Asn Ser Leu Ala Ile
 435 440 445
 Phe Leu Leu Ala Asn Leu Leu Thr Gly Ala Val Asn Leu Ser Ile Ser
 450 455 460
 Thr Ile Asp Ala Asn Thr Ala Gln Ala Ile Ala Val Leu Ile Gly Tyr
 465 470 475 480
 Ser Ser Ile Ile Thr Gly Val Ala Leu Ala Leu His His Ala Asn Ile
 485 490 495
 Lys Val Leu Pro Phe
 500

<210> 11
 <211> 1648
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <221> intron
 <222> (122)..(198)

<220>

<221> CDS

<222> (26)..(121)

<220>

<221> CDS

<222> (199)..(1608)

<400> 11

```
gcaaattcccg cggcattgag tcaag atg gat cca gat tat aaa gct cgc aaa 52
                               Met Asp Pro Asp Tyr Lys Ala Arg Lys
                               1                               5

gag gcc ttt gtc tca ggt ctt gca gga gga agc atc ctg gaa atc aac 100
Glu Ala Phe Val Ser Gly Leu Ala Gly Gly Ser Ile Leu Glu Ile Asn
 10                               15                               20                               25

gcc gtc acc ttg gtt gct tcg gttcgtgta ctatcttatt gtggctactt 151
Ala Val Thr Leu Val Ala Ser
                               30

cgccctacatt gtttctcgac taaccgagtc tcttttgcgat caatcag gta tcc gtt 207
                               Val Ser Val
                               35

ttt ctg tgg tca att cta caa tct cgc cta tcc ttt ttc aca ccc tac 255
Phe Leu Trp Ser Ile Leu Gln Ser Arg Leu Ser Phe Phe Thr Pro Tyr
          40                               45                               50

agc gcc gct gcc ctt ctc gtt gat ttc ctg ctc aat gta cta gct atc 303
Ser Ala Ala Ala Leu Leu Val Asp Phe Leu Leu Asn Val Leu Ala Ile
          55                               60                               65

ttg ttc gca acc act tta tac tct tcg gcg cct ctt ctt ctc aat ctc 351
Leu Phe Ala Thr Thr Leu Tyr Ser Ser Ala Pro Leu Leu Leu Asn Leu
          70                               75                               80

ctt cta ata tct ccc gct ctg ctg ata ctc ctc tct acg aaa cgt cct 399
Leu Leu Ile Ser Pro Ala Leu Leu Ile Leu Leu Ser Thr Lys Arg Pro
          85                               90                               95

cgg acc ccc gtc aaa gcg aaa cct cct cgc cag tcc gct aga gct ggg 447
Arg Thr Pro Val Lys Ala Lys Pro Pro Arg Gln Ser Ala Arg Ala Gly
100                               105                               110                               115

aaa gat gac tcg aaa cat gcg aca gcc ttg cca gag tct cta ccc att 495
Lys Asp Asp Ser Lys His Ala Thr Ala Leu Pro Glu Ser Leu Pro Ile
          120                               125                               130

cat cca ttt ctc acg aca tat cgc gcc gcc atg atg gtt atc acg tgc 543
His Pro Phe Leu Thr Thr Tyr Arg Ala Ala Met Met Val Ile Thr Cys
          135                               140                               145

atc gct atc ttg gct gtg gat ttt cgc att ttt cct cgc cga ttc gcc 591
Ile Ala Ile Leu Ala Val Asp Phe Arg Ile Phe Pro Arg Arg Phe Ala
          150                               155                               160

aag gta gaa aac tgg ggt aca tca ctc atg gat ctg ggc gtt gga tcg 639
Lys Val Glu Asn Trp Gly Thr Ser Leu Met Asp Leu Gly Val Gly Ser
          165                               170                               175
```

ttt gtc ttt tcg ggc gga gta gta tcc gct cgc tca cta ctc aag agc	687
Phe Val Phe Ser Gly Gly Val Val Ser Ala Arg Ser Leu Leu Lys Ser	
180 185 190 195	
agg acc aat ggc tct aaa agg ttg cct ctt gcc aag agg ttg att gcg	735
Arg Thr Asn Gly Ser Lys Arg Leu Pro Leu Ala Lys Arg Leu Ile Ala	
200 205 210	
tcg acg cga cac tct att cct ctg ctc gtc ctc ggc ctg att cgg cta	783
Ser Thr Arg His Ser Ile Pro Leu Leu Val Leu Gly Leu Ile Arg Leu	
215 220 225	
tac agc gtc aaa ggc ttg gac tat gcg gag cac gtc acc gag tac ggc	831
Tyr Ser Val Lys Gly Leu Asp Tyr Ala Glu His Val Thr Glu Tyr Gly	
230 235 240	
gta cat tgg aac ttc ttc ttt aca ttg ggt ctt ttg cct ccg ttc gtg	879
Val His Trp Asn Phe Phe Phe Thr Leu Gly Leu Leu Pro Pro Phe Val	
245 250 255	
gag gtc ttc gac gcc ttg gct acg atc att ccg tca tac gag gtt ctc	927
Glu Val Phe Asp Ala Leu Ala Thr Ile Ile Pro Ser Tyr Glu Val Leu	
260 265 270 275	
tcc gtg ggg atc gcc gtc ttg tat caa gtt gcc cta gag tca aca gac	975
Ser Val Gly Ile Ala Val Leu Tyr Gln Val Ala Leu Glu Ser Thr Asp	
280 285 290	
ttg aaa agc tac atc ctc gtc tcc cct cgt ggg cca agc tta ctg tcc	1023
Leu Lys Ser Tyr Ile Leu Val Ser Pro Arg Gly Pro Ser Leu Leu Ser	
295 300 305	
aag aat cgt gaa ggc gtc ttc tcc ttc tca ggt tat ctc gcg att ttt	1071
Lys Asn Arg Glu Gly Val Phe Ser Phe Ser Gly Tyr Leu Ala Ile Phe	
310 315 320	
ctt gct ggt cgt gcg atc ggc att cgg ata atc cct cgc gga act tct	1119
Leu Ala Gly Arg Ala Ile Gly Ile Arg Ile Ile Pro Arg Gly Thr Ser	
325 330 335	
ttc tca aga agc cca gaa cag gcc agg aga cgg gtc ctg atc agc ctt	1167
Phe Ser Arg Ser Pro Glu Gln Ala Arg Arg Arg Val Leu Ile Ser Leu	
340 345 350 355	
ggc gtg caa gcg tta gtg tgg acc act ctt ttt gtg ttg aac tcc act	1215
Gly Val Gln Ala Leu Val Trp Thr Thr Leu Phe Val Leu Asn Ser Thr	
360 365 370	
tat gcg atg gga tac gga gct aat atc cct gtc tcc cgc cgc ctc gct	1263
Tyr Ala Met Gly Tyr Gly Ala Asn Ile Pro Val Ser Arg Arg Leu Ala	
375 380 385	
aac atg ccc tat gtc ctt tgg gtt tcg gcg ttc aac acc gcg caa ctg	1311
Asn Met Pro Tyr Val Leu Trp Val Ser Ala Phe Asn Thr Ala Gln Leu	
390 395 400	
ttt gtg ttc tgc ctg atc gaa aca ctc tgc ttt cct gca gtt cat cgg	1359
Phe Val Phe Cys Leu Ile Glu Thr Leu Cys Phe Pro Ala Val His Arg	
405 410 415	
aca acg act caa gag agc gaa tct gag cga gtc gat ttt gct acg agc	1407

Thr Thr Thr Gln Glu Ser Glu Ser Glu Arg Val Asp Phe Ala Thr Ser
 420 425 430 435
 cga atc atg tcg gcc ttc aat aag aac agt ctc gcg atc ttt ctt ttg 1455
 Arg Ile Met Ser Ala Phe Asn Lys Asn Ser Leu Ala Ile Phe Leu Leu
 440 445 450
 gcc aat ctt ctg act gga gct gtg aat ctg agc atc tcc aca att gat 1503
 Ala Asn Leu Leu Thr Gly Ala Val Asn Leu Ser Ile Ser Thr Ile Asp
 455 460 465
 gct aat aca gcg cag gcc atc gct gtt ctc att gga tat tca tcc att 1551
 Ala Asn Thr Ala Gln Ala Ile Ala Val Leu Ile Gly Tyr Ser Ser Ile
 470 475 480
 atc aca ggg gtt gct cta gca ttg cat cat gcc aat atc aaa gta ctt 1599
 Ile Thr Gly Val Ala Leu Ala Leu His His Ala Asn Ile Lys Val Leu
 485 490 495
 cct ttc tag ggtatttacg agcaattggt ggtgtgttga agatatatag 1648
 Pro Phe
 500

<210> 12
 <211> 2045
 <212> DNA
 <213> *Cryptococcus neoformans*

<220>
 <221> intron
 <222> (137)..(198)

<220>
 <221> intron
 <222> (892)..(942)

<220>
 <221> intron
 <222> (1636)..(1686)

<220>
 <221> CDS
 <222> (44)..(2001)

<400> 12
 gtcatagcac taaatccccg ccataataag ctactgaatt gca atg ggg gat tac 55
 Met Gly Asp Tyr
 1

aag tcg gcc aaa gag gcc ttt gtc tcg gat aac cca ggt gct tct atc 103
 Lys Ser Ala Lys Glu Ala Phe Val Ser Asp Asn Pro Gly Ala Ser Ile
 5 10 15 20

tgg agt atc aac gct gtc agc ctg gtc gca ctg gtatgtagct cggttctccga 156
 Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu
 25 30

ggggttctgt catttggaga cgcttattaa ttgggatcgc ag gcg aca tat gct 210
 Ala Thr Tyr Ala
 35

ctc tgg atc gcc tta tcg ccg tac atc cgt cat gga ctc ctg aac aac	258
Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu Leu Asn Asn	
40 45 50	
tac ctg atc tgt gtt ctt ccc cta tta ttc ggg gtg acc atc ttc tca	306
Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr Ile Phe Ser	
55 60 65	
act tcg cct ctc gta ttt acc tct ttt ttg tcc att att tcc ctc gct	354
Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile Ser Leu Ala	
70 75 80	
ttc atc acg aaa tcc caa aaa tgc ttc aaa tct gtc agt tcg ccc gaa	402
Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser Ser Pro Glu	
85 90 95	
aag cca aaa ggc caa tgg cta gac gaa tca gac tcc gat gag gaa cca	450
Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp Glu Glu Pro	
100 105 110 115	
gcg gaa cct gct tct gca gct gga tct gca gca gtc tca cca gta aag	498
Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser Pro Val Lys	
120 125 130	
ctt cta cct tcc caa gtg gcg ttc gct tcg gga tcc cta tta tct ccc	546
Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu Leu Ser Pro	
135 140 145	
gat ccg aca aca tcc ccc atg tcg cca agt agt tct tca gct tca gga	594
Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ser Ala Ser Gly	
150 155 160	
cat gaa gac cct ttg ggg att atg ggc gtt aac aga cgg agg tcg cta	642
His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg Arg Ser Leu	
165 170 175	
tta gaa gga gtt tcg ctt gat gtt ccg tca cat atc gac tcc aag gtc	690
Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp Ser Lys Val	
180 185 190 195	
aga ata tct cct gtt ccc tac ttg agg ctc aaa aag tct agg gca acg	738
Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser Arg Ala Thr	
200 205 210	
aag gcg caa tgg gtg aaa gaa aag gga aga tta cca ttt ttg aca gtg	786
Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe Leu Thr Val	
215 220 225	
tac cga gcg cac atg atg ctc atg act gtt atc tgc atc ttg gcg gta	834
Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile Leu Ala Val	
230 235 240	
gat ttt gaa gtg ttt cct aga tgg cag ggc aag tgc gaa gat ttt ggt	882
Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu Asp Phe Gly	
245 250 255	
act agt ctg gtaagctttc cttcagccat ggtccagtgc tcaccgctct	931
Thr Ser Leu	
260	

acttgccgta g atg gac gtg ggt gtc ggg tca ttc gtc ttt tcc ctc ggt	981
Met Asp Val Gly Val Gly Ser Phe Val Phe Ser Leu Gly	
265 270 275	
ctc gtc tcc aca aaa tct ctt tct cct cca cct cca act cct acg ccc	1029
Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr Pro Thr Pro	
280 285 290	
tcc tcg ccc gct ctc aac tct cac atc att ccc ctc acc ccg tcc ccg	1077
Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr Pro Ser Pro	
295 300 305	
ttc act tcc atc ctc atc tcg ctc cga aaa tcc atc ccc atc ctc gtc	1125
Phe Thr Ser Ile Leu Ile Ser Leu Arg Lys Ser Ile Pro Ile Leu Val	
310 315 320	
ctc ggc ttt ata cgg ttg att atg gtc aag gga tct gat tat cct gag	1173
Leu Gly Phe Ile Arg Leu Ile Met Val Lys Gly Ser Asp Tyr Pro Glu	
325 330 335	
cat gtg acg gag tac ggc gtg cac tgg aat ttc ttc ttc acc ctc gca	1221
His Val Thr Glu Tyr Gly Val His Trp Asn Phe Phe Phe Thr Leu Ala	
340 345 350 355	
ttg gtt cct gtg ctc gcc gtg ggc att cga cca ttg acg cag tgg ctt	1269
Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr Gln Trp Leu	
360 365 370	
cgc tgg agt gtg ctt ggg gta atc atc tct ttg ctg cat cag ctg tgg	1317
Arg Trp Ser Val Leu Gly Val Ile Ile Ser Leu Leu His Gln Leu Trp	
375 380 385	
tta aca tat tat ctc caa tcc atc gtc ttc tca ttc ggc cgg tca ggt	1365
Leu Thr Tyr Tyr Leu Gln Ser Ile Val Phe Ser Phe Gly Arg Ser Gly	
390 395 400	
atc ttt cta gca aac aag gaa ggc ttc tcc tct ctt cct ggt tat ctt	1413
Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro Gly Tyr Leu	
405 410 415	
tcc ata ttt ttg atc ggc ttg tct att gga gat cat gtt tta agg ctc	1461
Ser Ile Phe Leu Ile Gly Leu Ser Ile Gly Asp His Val Leu Arg Leu	
420 425 430 435	
agt tta cca cca aga aga gag agg gtc gtg tca gaa aca aat gaa gag	1509
Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr Asn Glu Glu	
440 445 450	
cat gag cag agt cat ttt gag aga aaa aaa ttg gat ttg att atg gag	1557
His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu Ile Met Glu	
455 460 465	
ttg att gga tat agc tta ggc tgg tgg gca ctc tta gga ggc tgg att	1605
Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly Gly Trp Ile	
470 475 480	
tgg gcc ggc ggg gag gta tcc agg cgt tta gtaagtggac atctttggta	1655
Trp Ala Gly Gly Glu Val Ser Arg Arg Leu	
485 490	
atattgtacc tataactaatc cctgcataaa g gcc aac gct cct tat gta ttt	1707

	Ala	Asn	Ala	Pro	Tyr	Val	Phe	
	495						500	
tgg gta gcg gca tac aat acc acc ttt ctc ctc ggc tac ctc ctc ctt								1755
Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly Tyr Leu Leu Leu								
	505						515	
acc cac att att cca tct ccc acc tct tcc caa aca tca cca tcg atc								1803
Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr Ser Pro Ser Ile								
	520						530	
tta gtg cct ccc ttg ctc gac gct atg aat aaa aac ggt ctc gcg ata								1851
Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn Gly Leu Ala Ile								
	535						545	
ttt ttg gcg gcc aac ttg ctt aca gga ctg gtg aat gtg agc atg aag								1899
Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn Val Ser Met Lys								
	550						560	
aca atg tat gcg ccg gcg tgg ttg tca atg ggg gtg tta atg ttg tat								1947
Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val Leu Met Leu Tyr								
	565						575	580
acc ttg aca atc agt tgt gta ggg tgg ata ctg aaa gga cgg agg atc								1995
Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys Gly Arg Arg Ile								
	585						595	
aag ata tagttaaagt gtttaccatg caggatactg agtatctcgg ttca								2045
Lys Ile								

<210> 13
 <211> 1797
 <212> DNA
 <213> *Cryptococcus neoformans*

<220>
 <221> CDS
 <222> (1)..(1794)

<400> 13																	
atg ggg gat tac aag tcg gcc aaa gag gcc ttt gtc tcg gat aac cca																	48
Met Gly Asp Tyr Lys Ser Ala Lys Glu Ala Phe Val Ser Asp Asn Pro																	
1 5 10 15																	
ggg gct tct atc tgg agt atc aac gct gtc agc ctg gtc gca ctg gcg																	96
Gly Ala Ser Ile Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu Ala																	
	20						25					30					
aca tat gct ctc tgg atc gcc tta tcg ccg tac atc cgt cat gga ctc																	144
Thr Tyr Ala Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu																	
	35						40					45					
ctg aac aac tac ctg atc tgt gtt ctt ccc cta tta ttc ggg gtg acc																	192
Leu Asn Asn Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr																	
	50						55					60					
atc ttc tca act tcg cct ctc gta ttt acc tct ttt ttg tcc att att																	240
Ile Phe Ser Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile																	
	65						70					75					80

tcc ctc gct ttc atc acg aaa tcc caa aaa tgc ttc aaa tct gtc agt	288
Ser Leu Ala Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser	
85 90 95	
tcg ccc gaa aag cca aaa ggc caa tgg cta gac gaa tca gac tcc gat	336
Ser Pro Glu Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp	
100 105 110	
gag gaa cca gcg gaa cct gct tct gca gct gga tct gca gca gtc tca	384
Glu Glu Pro Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser	
115 120 125	
cca gta aag ctt cta cct tcc caa gtg gcg ttc gct tcg gga tcc cta	432
Pro Val Lys Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu	
130 135 140	
tta tct ccc gat ccg aca aca tcc ccc atg tcg cca agt agt tct tca	480
Leu Ser Pro Asp Pro Thr Ser Pro Met Ser Pro Ser Ser Ser	
145 150 155 160	
gct tca gga cat gaa gac cct ttg ggg att atg ggc gtt aac aga cgg	528
Ala Ser Gly His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg	
165 170 175	
agg tcg cta tta gaa gga gtt tcg ctt gat gtt ccg tca cat atc gac	576
Arg Ser Leu Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp	
180 185 190	
tcc aag gtc aga ata tct cct gtt ccc tac ttg agg ctc aaa aag tct	624
Ser Lys Val Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser	
195 200 205	
agg gca acg aag gcg caa tgg gtg aaa gaa aag gga aga tta cca ttt	672
Arg Ala Thr Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe	
210 215 220	
ttg aca gtg tac cga gcg cac atg atg ctc atg act gtt atc tgc atc	720
Leu Thr Val Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile	
225 230 235 240	
ttg gcg gta gat ttt gaa gtg ttt cct aga tgg cag ggc aag tgc gaa	768
Leu Ala Val Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu	
245 250 255	
gat ttt ggt act agt ctg atg gac gtg ggt gtc ggg tca ttc gtc ttt	816
Asp Phe Gly Thr Ser Leu Met Asp Val Gly Val Gly Ser Phe Val Phe	
260 265 270	
tcc ctc ggt ctc gtc tcc aca aaa tct ctt tct cct cca cct cca act	864
Ser Leu Gly Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr	
275 280 285	
cct acg ccc tcc tcg ccc gct ctc aac tct cac atc att ccc ctc acc	912
Pro Thr Pro Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr	
290 295 300	
ccg tcc ccg ttc act tcc atc ctc atc tcg ctc cga aaa tcc atc ccc	960

Pro 305	Ser	Pro	Phe	Thr	Ser 310	Ile	Leu	Ile	Ser	Leu 315	Arg	Lys	Ser	Ile	Pro 320	
atc Ile	ctc Leu	gtc Val	ctc Leu	ggc Gly 325	ttt Phe	ata Ile	cgg Arg	ttg Leu	att Ile	atg Met	gtc Val	aag Lys	gga Gly	tct Ser	gat Asp	1008
tat Tyr	cct Pro	gag Glu	cat His 340	gtg Val	acg Thr	gag Glu	tac Tyr	ggc Gly 345	gtg Val	cac His	tgg Trp	aat Asn	ttc Phe	ttc Phe	ttc Phe	1056
acc Thr	ctc Leu	gca Ala 355	ttg Leu	gtt Val	cct Pro	gtg Val	ctc Leu	gcc Ala 360	gtg Val	ggc Gly	att Ile	cga Arg	cca Pro	ttg Leu	acg Thr	1104
cag Gln	tgg Trp	ctt Leu	cgc Arg	tgg Trp	agt Ser	gtg Val	ctt Leu	ggg Gly 375	gta Val	atc Ile	atc Ile	tct Ser	ttg Leu	ctg Leu	cat His	1152
cag Gln 385	ctg Leu	tgg Trp	tta Leu	aca Thr	tat Tyr 390	tat Tyr	ctc Leu	caa Gln	tcc Ser	atc Ile 395	gtc Val	ttc Phe	tca Ser	ttc Phe	ggc Gly 400	1200
cgg Arg	tca Ser	ggt Gly	atc Ile	ttt Phe 405	cta Leu	gca Ala	aac Asn	aag Lys	gaa Glu 410	ggc Gly	ttc Phe	tcc Ser	tct Ser	ctt Leu	cct Pro 415	1248
ggc Gly	tat Tyr	ctt Leu	tcc Ser 420	ata Ile	ttt Phe	ttg Leu	atc Ile	ggc Gly 425	ttg Leu	tct Ser	att Ile	gga Gly	gat Asp	cat His	gtt Val	1296
tta Leu	agg Arg	ctc Leu	agt Ser	tta Leu	cca Pro	cca Pro	aga Arg	aga Arg	gag Glu	agg Arg	gtc Val	gtg Val	tca Ser	gaa Glu	aca Thr	1344
aat Asn 450	gaa Glu	gag Glu	cat His	gag Glu	cag Gln	agt Ser	cat His	ttt Phe	gag Glu	aga Arg	aaa Lys	aaa Lys	ttg Leu	gat Asp	ttg Leu	1392
att Ile 465	atg Met	gag Glu	ttg Leu	att Ile	gga Gly	tat Tyr	agc Ser	tta Leu	ggc Gly	tgg Trp	tgg Trp	gca Ala	ctc Leu	tta Leu	gga Gly 480	1440
ggc Gly	tgg Trp	att Ile	tgg Trp	gcc Ala 485	ggc Gly	ggg Gly	gag Glu	gta Val	tcc Ser	agg Arg	cgt Arg	tta Leu	gcc Ala	aac Asn	gct Ala 495	1488
cct Pro	tat Tyr	gta Val	ttt Phe	tgg Trp	gta Val	gcg Ala	gca Ala	tac Tyr	aat Asn	acc Thr	acc Thr	ttt Phe	ctc Leu	ctc Leu	ggc Gly	1536
tac Tyr	ctc Leu	ctc Leu	ctt Leu	acc Thr	cac His	att Ile	att Ile	cca Pro	tct Ser	ccc Pro	acc Thr	tct Ser	tcc Ser	caa Gln	aca Thr	1584
tca Ser 530	cca Pro	tcg Ser	atc Ile	tta Leu	gtg Val	cct Pro	ccc Pro	ttg Leu	ctc Leu	gac Asp	gct Ala	atg Met	aat Asn	aaa Lys	aac Asn	1632
ggc Gly	ctc Leu	gcg Ala	ata Ile	ttt Phe	ttg Leu	gcg Ala	gcc Ala	aac Asn	ttg Leu	ctt Leu	aca Thr	gga Gly	ctg Leu	gtg Val	aat Asn	1680

545	550	555	560	
gtg agc atg aag aca atg tat gcg ccg gcg tgg ttg tca atg ggg gtg				1728
Val Ser Met Lys Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val				
	565	570	575	
tta atg ttg tat acc ttg aca atc agt tgt gta ggg tgg ata ctg aaa				1776
Leu Met Leu Tyr Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys				
	580	585	590	
gga cgg agg atc aag ata tag				1797
Gly Arg Arg Ile Lys Ile				
	595			

<210> 14
 <211> 598
 <212> PRT
 <213> *Cryptococcus neoformans*

<400> 14
 Met Gly Asp Tyr Lys Ser Ala Lys Glu Ala Phe Val Ser Asp Asn Pro
 1 5 10 15
 Gly Ala Ser Ile Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu Ala
 20 25 30
 Thr Tyr Ala Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu
 35 40 45
 Leu Asn Asn Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr
 50 55 60
 Ile Phe Ser Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile
 65 70 75 80
 Ser Leu Ala Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser
 85 90 95
 Ser Pro Glu Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp
 100 105 110
 Glu Glu Pro Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser
 115 120 125
 Pro Val Lys Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu
 130 135 140
 Leu Ser Pro Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ser
 145 150 155 160
 Ala Ser Gly His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg
 165 170 175
 Arg Ser Leu Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp
 180 185 190
 Ser Lys Val Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser
 195 200 205
 Arg Ala Thr Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe

210	215	220
Leu Thr Val Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile 225 230 235 240		
Leu Ala Val Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu 245 250 255		
Asp Phe Gly Thr Ser Leu Met Asp Val Gly Val Gly Ser Phe Val Phe 260 265 270		
Ser Leu Gly Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr 275 280 285		
Pro Thr Pro Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr 290 295 300		
Pro Ser Pro Phe Thr Ser Ile Leu Ile Ser Leu Arg Lys Ser Ile Pro 305 310 315 320		
Ile Leu Val Leu Gly Phe Ile Arg Leu Ile Met Val Lys Gly Ser Asp 325 330 335		
Tyr Pro Glu His Val Thr Glu Tyr Gly Val His Trp Asn Phe Phe Phe 340 345 350		
Thr Leu Ala Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr 355 360 365		
Gln Trp Leu Arg Trp Ser Val Leu Gly Val Ile Ile Ser Leu Leu His 370 375 380		
Gln Leu Trp Leu Thr Tyr Tyr Leu Gln Ser Ile Val Phe Ser Phe Gly 385 390 395 400		
Arg Ser Gly Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro 405 410 415		
Gly Tyr Leu Ser Ile Phe Leu Ile Gly Leu Ser Ile Gly Asp His Val 420 425 430		
Leu Arg Leu Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr 435 440 445		
Asn Glu Glu His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu 450 455 460		
Ile Met Glu Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly 465 470 475 480		
Gly Trp Ile Trp Ala Gly Gly Glu Val Ser Arg Arg Leu Ala Asn Ala 485 490 495		
Pro Tyr Val Phe Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly 500 505 510		
Tyr Leu Leu Leu Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr 515 520 525		
Ser Pro Ser Ile Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn		

530

535

540

Gly Leu Ala Ile Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn
 545 550 555 560

Val Ser Met Lys Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val
 565 570 575

Leu Met Leu Tyr Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys
 580 585 590

Gly Arg Arg Ile Lys Ile
 595

<210> 15

<211> 35

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 15

ggaattcatg tcgactttaa aacagagaaa agagg

35

<210> 16

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 16

gcacgcattt atagcttaat gaatattcctt tttctatac

39

<210> 17

<211> 60

<212> DNA

<213> Saccharomyces cerevisiae

<400> 17

atggcaacag tacatcagga gaatatgtcg acttttaaacc cggatccccg tcgttttaaacc 60

<210> 18

<211> 60

<212> DNA

<213> Saccharomyces cerevisiae

<400> 18

ttatagctta atgaatattc tttttctata caagaaaacc gaattcgagc tcgttttaaacc 60